

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 09:57:31 ; Search time 2016.58 Seconds

(without alignments)
3628.854 Million cell updates/sec

Title: US-09-602-833a-3

Perfect score: 681
Sequence: 1 atgagaaatcgcgatactgc.....ctttagcctcaatttga 681

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	493.8	72.5	1450	12	AK010252	Mus muscu
2	367.6	54.0	526	10	AA416235	VF38D07.T
3	323.2	47.5	483	10	AA422330	VF45B09.T
4	246.6	36.2	557	10	BE110536	UI-R-BJ1-
5	237.4	34.9	462	13	AO729142	HS-5467_B
6	168	24.7	432	10	AA488294	UI-M-BH3-
7	167	24.5	443	10	AA500912	VG03404.T
8	148.2	21.8	377	11	BG203142	RST22516
9	138	20.3	370	11	BG197958	RST17210
10	137.8	20.2	598	11	AO670712	HS-5449_A
11	135	19.8	508	11	BG210970	RST30524
12	134.2	19.7	560	13	AA427288	CITBI-EL-

c	13	134.2	19.7	572	13	AA427239	CITBI-EL-
14	125	18.4	470	10	AL120256	DKF2P761J	
15	125	18.4	669	10	AL133928	DKF2P761J	
c	16	119.6	17.6	589	13	AZ412330	1M0185C13
17	99	14.5	446	10	AA417843	ZV01C02.T	
c	18	91.4	13.4	470	13	AZ412322	1M0185A15
c	19	88.4	13.0	453	13	AO791237	HS-5495_A
c	20	86.8	12.7	366	10	AA446687	ZW84B08.T
c	21	83	12.2	794	10	AV700252	AV700252
22	76.4	11.2	194	10	AA149346	Z029C11.T	
23	75.4	11.1	424	11	BG359014	BOVMS1-02	
24	65.6	9.6	298	11	BF840611	MRI-HT106	
25	64.8	9.5	650	10	AA799431	EST188928	
c	26	64	9.4	377	10	AI339758	AI339758
27	63.8	9.4	1245	12	AK006601	Nus muscu	
28	59.4	8.7	422	10	AA432886	VG89C04.T	
29	59.4	8.7	450	11	BF545892	UI-R-BT0-	
30	59.2	8.7	525	11	BF077050	226844_MA	
31	57.4	8.4	826	11	BF344653	602015293	
32	57.4	8.4	876	11	BG682195	602629502	
33	56.4	8.3	772	10	AU123287	AU123287	
34	56.2	8.3	911	11	BG360067	602371653	
35	55.4	8.1	369	10	AA418446	56312_MAR	
36	55	8.1	419	10	AI106485	CB03C01.T	
37	54.8	8.0	868	11	BF670880	602149967	
38	54.4	8.0	809	10	AL520588	AL520588	
39	54.2	8.0	354	11	W75647	me49B12.T	
40	54.2	8.0	400	10	AI385903	me49B12.Y	
41	54.2	8.0	567	10	BE664685	152497_MA	
42	53.2	7.8	586	10	AA662786	SWYD25CAU	
43	52.8	7.8	510	10	AW918885	EST350189	
44	52.8	7.8	613	10	AA441056	LD15830.5	
45	52.6	7.7	317	10	AA483293	52416_MAR	

ALIGNMENTS

RESULT 1	AK010252	1450 bp	mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2400002D05, full insert sequence.	HTC	05-JUL-2001
LOCUS	AK010252				
DEFINITION	AK010252				
ACCESSION	AK010252.1	GI:12845555			
VERSION	AK010252.1	GI:12845555			
KEYWORDS	CAP trapper.				
SOURCE	Mus musculus (strain:C57BL/6J) ES cells cDNA to mRNA, clone:lib:RIKEN full-length enriched mouse cDNA library clone:2400002D05.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
AUTHORS	1 (bases 1 to 1450) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Methods in enzymology. 303, 19-44 (1999)				
REFERENCE	99279253				
MEDLINE	99279253				
PUBMED	10349636				
AUTHORS	2 (bases 1 to 1450) Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome research. 10 (10), 1617-1630 (2000)				
TITLE	11042159				
JOURNAL	20499374				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3 (bases 1 to 1450)				
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J.,				

TITLE	Oikazaki,Y., Muramatsu,M., Inoue,Y., Kirr,A. and Hayashizaki,Y. Riken Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome research. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4 (bases 1 to 1450) The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
AUTHORS	Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5 (bases 1 to 1450) Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Carninci,P., Fukuda,S., Fukushima,Y., Furuno,M., Hannagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Horii,F., Imotoh,K., Ishii,Y., Itoh,M., Itama,H., Kato,H., Kawaji,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishii,K., Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toyota,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suheiho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gscc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
FEATURES	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGACAGACATCCAGACGCCTTTTGTTCCTTTTTCVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GACAGAGACTTCGACGTAATTAAATTAATCATCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: xhoI; 3' end: SstI. Host: T.O.R.
SOURCE	Location/Qualifiers 1..1450 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /db_xref="MGD:MGI:1907395" /db_xref="MGD:MGI:1921499" /cclone="2400002D05" /cell_type="ES cells" /cloned_lib="RIKEN full-length enriched mouse cDNA library" size..1269 note="putative" /protein_start=1 /protein_id="BA826797.1" /db_xref="GI:12845556" /translation="MGKHYVVPDISYRALMETRYKKHKAKWQKEARERLEKSLEKIK EBMDFAECRRKGVPQAECKNGEVDSITSLRLKEIENSVSRSARVKDKDRSPV FEISGTQMKELPDLSEKQTLKEMYSISTLIQLIPYTELFQAMKILDPKNQITCP AEGIRLNLKELNVEFNHLKSIPELDGCHLEBIDCSGMILMDLPFLSNLKQYF VDLSANKESSVPICVLKRWLMIDISSNNLSDLPQIDBLELEGLGFIYKKNLTLYP QAALNKTKTLLYVSGDHLYEPFDALCDASTPLKPYSLVNPIDKTGCGDTEDTVASE RDROHFDEKPEMKAYIEDLKEREAIVPSPTLVVSPSLQ"
CDS	415 a 304 c 367 g 364 t
BASE COUNT	
ORIGIN	

[illegible]

QY 205 aagcaagttacattgttagatatactcgaacaagaagtttccagtgctcccaatctgttc 264
|||||
Db 120 AAGCAAGTTACATTGTGGATATCTCTCGAACAAGTTCTCCAGCGTTCTATCTGTGTC 179
|||||
QY 265 ctggagagtgctgaatttcagtggttgatatacagcagaataaaccctgacgtgcg 324
|||||
Db 180 CTGCGAGTGTCTGCTCAGTGGCTGTGATACACACCAACAACTGATGACCTGCA 239
|||||
QY 325 caagatatagacaggtctgagagctgagagcttctcttgatataaacaagtgc 384
|||||
Db 240 CAAGTATAGACAGCGCTGGAAGAGCTACAGTTCTCTGCTATATAAACAAGCTGAC 299
|||||
QY 385 taacctccattccatgctgaacctgaagaagctcctgtagtgcagtgaggac 444
|||||
Db 300 TACCTTCTCAAGCATCTCAACCTCAAAAAGCTCACCTTGCTGTGTCAGTGGGAT 359
|||||
QY 445 catttgaggagctcccaagctgcttgtagctatccacaaccttaaatgtgac 504
|||||
Db 360 CACCTGTGAGAGTCCGACGCGCTCTGCGATGCTCCACGCTTTGAATTTGTAGC 419
|||||
QY 505 ctatgacaatccatctatgataatgccaatgtgagaatgcaatgaataatgaagt 564
|||||
Db 420 CTGTGACATCCCATTTGATATAGACCGGATGTCAAGACACTGAGACAGTAGAGAC 479
|||||
QY 565 gaac 568
|||
Db 480 GAGC 483
|||

RESULT 4
BE110536/c mRNA EST 13-JUN-2000
LOCUS BE110536 557 bp
DEFINITION UI-R-BJ1-avt-b-09-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
UI-R-BJ1-avt-b-09-0-UI 3', mRNA sequence.
ACCESSION BE110536
VERSION BE110536.1 GI:8502641
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 557)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized heart library cDNA Library Preparation: M.B. Soares Lab
Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 Forward
POLA-yes. Location/Qualifiers
1..557
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ1-avt-b-09-0-UI"
/clone_1b="UI-R-BJ1"

/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1
library is a subtracted library derived from the following
tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,
AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.
For a detailed description of the library from which this
clone was derived, please visit our web site at
rategen.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_Lib-UI-R-BJ1
TAG_Tissue-heart
TAG_SEQ-ACAAC"

BASE COUNT 136 a 104 c 139 g 177 t 1 others
ORIGIN

Query Match 36.2%; Score 246.6; DB 10; Length 557;
Best Local Similarity 81.8%; Pred. No. 5.7e-56;
Matches 296; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

QY 320 tgcgcaagatatagacagctagagagctgcagagcttctctgtataaacaagt 379
|||||
Db 557 TGCCACAAGATATAGACAGCTGGAAGAGCTACA-AGTTTCTCTGTATAAAAACAAGC 499
|||||
QY 380 tgacctaccctccattccatctcgaacctgaagaagctcaactctgttagctgcaqtg 439
|||||
Db 498 TGACCTACTTCTCCTCAACCATGCTCAACGCTCAAAACTCACCTGCTGTGTCATG 439
|||||
QY 440 gggaccattgtgtgagctcccaactgccccttgtagctatccacaacctttaaattg 499
|||||
Db 438 GGGATGACCTGTGTGAGCTCCCGACCGCCCTNTGCGATGCTCCACGCTTTGAATTTG 379
|||||
QY 500 taagccttatgtgacaatctctatgataatgccaatgtgagaatgagcaatgaataatgg 559
|||||
Db 378 TAAAGCTTTTGACATCCATCCATGTGACAGACCGGTCAGACACTGACACACAGTAG 319
|||||

QY 560 aaagtgaacggatgcgaacaatttgataagaagtatgaagcctatatitgaagac 619
|||||
Db 318 AAGCGAAGACAGACCGCGACGCTTGATAGAAATTATGAAACATACATCGAAGAC 259
|||||

QY 620 ttaagaagaagaatctgttccagctataccacaagaatgctttagcctcaactt 679
|||||
Db 258 TTAAGAAGAAGAAGCTGTCTCCAGTATACCGCAAGTGTATTAGCTTCAACTTT 199
|||||

QY 680 ga 681
|||
Db 198 GA 197
|||

RESULT 5
A0729142 462 bp DNA GSS 15-JUL-1999
LOCUS HS_5467.B2.B10.SP6E.RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate=1043 Col=20 Row=D, DNA sequence.
ACCESSION A0729142
VERSION A0729142.1 GI:5500694
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 462)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCL-11. For BAC library availability, please contact Pieter de Jong (pieter@edj.med.buffalo.edu). Clones may be purchased from BACAC Resources (<http://bacpac.med.buffalo.edu/ordering/Bac.htm>) or from Research Genetics (<http://www.hsc.washington.edu>) Plate: 1043 row: D column: 20

Seq primer: SP6
Class: BAC ends
High quality sequence stop: 462.

FEATURES

source

1. .462
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate:1043 Col=20 Row=D"
/clone_lib="RPCL-11 Human Male BAC Library"
/sex="male"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

BASE COUNT 108 a 127 c 92 g 135 t

ORIGIN

Query Match

Best Local Similarity 34.9%; Score 237.4; DB 13; Length 462;

Matches 293; Conservative 0; Mismatches 51; Indels 5; Gaps 2;

QY 170 aataatgagctgcctctgaattgaattgaagcaagttatgtatgatatct 229
DB 5 AATTCACAGAGCTGCTCTGATTAAGTATGGAAGCCAGTGCATGATACATATC 64
QY 230 cagcaacaagtttccagtgtcccaatctgtctctgagatgtcgaatttcagtgt 289
DB 65 CACCAACAAGTTTCCAGTGTCCACTGTCCTGAGAGATGC-TATTCTCACTGCT 123
QY 290 tggatatacagcaacaatacctgaccgacctgcgcaagatatagacagctagagagc 349
DB 124 TGGATATCAGCAACATTAACCTGACCTGCTGGGGAAGT-----ACAGCTGGAAGAGC 179
QY 350 tgcagagcttctctgtataaacaagttgacctacttccctattccatgtcgaac 409
DB 180 CGAGAGGCTTCTCTGTATAGAACAGGTGACCTACCTGCTTACCCCATGCTGAC 239
QY 410 tgaagaagctcactctgttagtgcgtgagggagacattgtgtgagctcccaatgcc 469
DB 240 TGAAGAAGGACACCTTTAGTGTCAATGAGGAGCACCTGGAGCTTCAACCTGCTC 299
QY 470 ttgttactcatcacacaccttaaaattgttaagccttatgacacatcc 518
DB 300 TTTGTACTCAGTCACACCTTTAAATTGTCTAAGCCTTATAACATCC 348

RESULT 6

AM488294/c

LOCUS 432 bp mRNA

DEFINITION UI-M-BH3-ary-h-06-0-UI.s1 NIH_BMAP_M.S4 Mus musculus cDNA clone

ACCESSION AM488294

VERSION AM488294.1

KEYWORDS GI:7058564

SOURCE EST.

ORGANISM house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 432)
Bonaldo, M.F., Lennon, G., and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL

97044477

Medline

COMMENT

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COMMENT

Query Match	24.5%;	Score 167;	DB 10;	Length 443;
Best Local Similarity	80.8%;	Pred. No. 1.5e-34;		
Matches 219;	Conservative 0;	Mismatches 50;	Indels 2;	Gaps 2;
QY 413	agaagctactctgttattgctgctggtgggaccaatttggtga-gctcccaacgacctt	471		
Db 1	AAAAGCTCACCTGCTGGTTGTCAAGTGGGATCAACCTGTGTGACGCTCCACACGCTTC	60		
QY 472	tgtacatccacacacaccttaaatltttaaagccttaaggacaatccatctgataatgcc	531		
Db 61	TGCGATGCTCCTCAGCCCTTTGAATTTTAAAGCCTTGTGGCAATCCATGATTAAGACC	120		
QY 532	caatgtgaagatgycgaatgaataatggaagaatgaaagcggatcgccaac-attgtataa	590		
Db 121	GGATGTCAAGACACTGAAGACACAGTAGAGAGCGAGCCGACCGCATTTTGATTA	180		
QY 551	agaagttgaagaagcctataatggaagaccttaagaagaagaatctgttccagctatac	650		
Db 181	GGATTATTATGAAGCATATTATTGAAGACCTTAAGAAAGAAAGAAAGCTGTCCAGTTATAC	240		
QY 651	caaccaagctgcttttagccttcaacttga	681		
Db 241	GACCAAGTGTCAATTAGTCTTCACCTTGA	271		
RESULT 8				
LOCUS BG203142	377 bp	mRNA	EST	21-Apr-2001
DEFINITION R5722516	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	
ACCESSION BG203142				
VERSION BG203142.1	GI:13724829			
KEYWORDS EST.				
SOURCE human.				
ORGANISM Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE 1 (bases 1 to 377)				
AUTHORS Harrington,J.J., Sherif,B., Rundlett,S., Jackson,P.D., Perry,R.,				
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,				
Lerner,L., Krashinsky,D., McElligott,K., Clark,S., Mays,R., Smith,E.,				
Veloso,N., Hess,J.J., Colgren,K., Lo,K., Offenbacher,U., Danzig,J.,				
and Ducar,M.				
TITLE Creation of Genome-wide Protein Expression Libraries using Random				
JOURNAL Activation of Gene Expression				
COMMENT Nat. Biotechnol. 19 (5), 440 (2001) In press				
CONTACT Scott J. Cain				
Athersys, Inc.				
3201 Carnegie Ave, Cleveland, OH 44115, USA				
Tel: 216 431 9900				
Fax: 216 361 9596				
Email: scain@atersys.com				
FEATURES				
SOURCE				
1.377				
/organism="Homo sapiens"				
/db_xref="taxon:9606"				
/clone_lib="Athersys RAGE Library"				
/cell_line="HT1080"				
/note="See 'Creation of Genome-wide Protein Expression				
Libraries using Random Activation of Gene Expression',				
Nature Biotechnology, in press. Note that even though the				
cell type indicated is HT1080, since a random activation				
method was used, these sequence tags are not necessarily				
expressed in HT1080 under normal circumstances."				
BASE COUNT 139 a 66 c 65 g 104 t 3 others				
ORIGIN				
Query Match	21.8%;	Score 148.2;	DB 11;	Length 377;

RESULT 11
Bg210970 508 bp mRNA EST 21-APR-2001
LOCUS Bg210970.1
DEFINITION R3730524 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION Bg210970
VERSION Bg210970.1 GI:13732657
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Krasnoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
Velasco,N., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J.
and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using Random
Activation of Gene Expression
JOURNAL Nat. Biotechnol. 19 (5), 440 (2001) In press
COMMENT Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 508.
Location/Qualifiers
1..508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, In press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 182 a 81 c 83 g 160 t
ORIGIN
Query Match 19.8%; Score 135; DB 11; Length 508;
Best Local Similarity 98.1%; Pred. No. 6.5e-26;
Matches 157; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Oy 522 tgaataaccgaatgtgaagatggaatgaataatgaagaatggaacggaatcgcaaca 581
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Db 33 TGNATATCCCAATGTG-AGATGGCAATGAAT-ATGGAAAGTGAACGGGATCGCCACA 90
Oy 582 ttctgataaagaagttatgaagcctatctgaagacctaagaagaagaatctgttc 641
|||
Db 91 TTTTGATTAAGAGTTATGAAGACCTATATGAAGACCTTAAGAAGAAGATCTGTTC 150
Oy 642 cagctataccaccaaagtgcttttaagcctcaacttga 681
|||
Db 151 CAGCTATACACCAAGTGTCTTTTGAAGCTTCAACTTGA 190
RESULT 12
A0427288/c 560 bp DNA GSS 24-MAR-1999
LOCUS A0427288
DEFINITION CITBI-El-2568D1.TR CITBI-El Homo sapiens genomic clone 2568D1, DNA
sequence.
ACCESSION A0427288
VERSION A0427288.1 GI:4500038
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 560)

AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other-GSSs: CITBI-El-2568D1.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hwe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
Location/Qualifiers
1..560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2568D1"
/clone_lib="CITBI-El"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 132 a 154 c 101 g 173 t
ORIGIN
Query Match 19.7%; Score 134.2; DB 13; Length 560;
Best Local Similarity 91.6%; Pred. No. 1.1e-25;
Matches 153; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
Oy 1 atgagaattcggatctcccaaaaacaaatctcaactctccgcaggaatggtgt 60
|||
Db 167 ATGAGAAATTCAGATCTCCCAAGAACAAATCTCAGATTTCCAGCTAACTCAGTTGT 108
Oy 61 ttgaagaccctgaagaagactcaatgtgggttcaactatctgaagaagcattccctcagaa 120
|||
Db 107 TTGAAGACCTGAAATTAATCAATGTGATTCACACTATCGAAGAGCATTCCTCAAG 48
Oy 121 ttggagaattgtgaatctagagagactgattgtctggaact 167
|||
Db 47 CTGGGAGATTGTG-AAATCTAGAGGAGGACTGATTGTCTGGAATCT 2
RESULT 13
A0427239/c 572 bp DNA GSS 24-MAR-1999
LOCUS A0427239
DEFINITION CITBI-El-2568B9.TR CITBI-El Homo sapiens genomic clone 2568B9, DNA
sequence.
ACCESSION A0427239
VERSION A0427239.1 GI:4499942
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other-GSSs: CITBI-El-2568B9.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200

Fax: 301 838 0208
Email: hbe@ligr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page: http://www.ligr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES

Location/Qualifiers
1..572

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2568B9"
/clone_lib="CITRI-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOBAcl1; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC library D"
BASE COUNT 134 a 157 c 104 g 177 t
ORIGIN

Query Match 19.7%; Score 134.2; DB 13; Length 572;
Best Local Similarity 91.6%; Pred. No. 1.1e-25;
Matches 153; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

OY 1 atggaattcttgatctgcacaaaccacatctcacatcttcacagcagaatcgattgt 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 167 ATGGAATTTCAGATCTGCCAAGACAAATCTCACATTTTCCAGCTAAACTAGTTGT 108
OY 61 ttgaagaacctgaagaactcaatgatgtgttcaactatctgaagaacatctccacgaa 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 107 TTGAAGAACCCTGAATATCAATGATGAGTTTCAACTATCTGAAGAGATTCCTCCAGAG 48
OY 121 ttgggaatgttgaaatctagagagactgtgatgttcttgaaatct 167
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Db 47 CTGGGAGATTGTG-AAATCTAGAGGACTGTGATTGTTCTGGAAATCT 2

RESULT 14

AL120256 470 bp mRNA EST 25-FEB-2000
LOCUS DKEZP761J017_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
DEFINITION DKEZP761J017 5', mRNA sequence.
ACCESSION AL120256
VERSION AL120256.1 GI:5926155
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL 1 (bases 1 to 470)
COMMENT Koehler K., Beyer A., Mewes H.W., Gassenhuber J. and Wiemann S.
EST (Koehler, et al.)
Unpublished (1999)
CONTACT: Koehler K
MIPS

Am Klopferpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.

This clone (DKEZP761J017) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

FEATURES

source

1..470
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKEZP761J017"
/clone_lib="761 (synonym: hamy2)"

/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 166 a 73 c 77 g 150 t 4 others
ORIGIN

Query Match 18.4%; Score 125; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 3.1e-23;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 tggaaagtgaacggatcgccacatttgaataaagaattgaagcctatataga 616
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Db 1 TGGAAAGGAGACGGATCGCCACATTTTGATTAAGAAGTATGAACCTATATGAG 60
OY 617 acctaaagaagaagatctgtccacgtatcacaccacaaagtcttttagccttcac 676
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 ACCTTAAGAAGAAGAAATCTGTCCACGCTATACACCAAGTGCTTTAGCCTCAAC 120
OY 677 ttga 681
|||||
Db 121 TTGA 125

RESULT 15

AL133928 669 bp mRNA EST 25-FEB-2000
LOCUS DKEZP761O1814_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
DEFINITION DKEZP761O1814 5', mRNA sequence.
ACCESSION AL133928
VERSION AL133928.1 GI:6602115
KEYWORDS EST.
SOURCE human.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL 1 (bases 1 to 669)
COMMENT Ansoerge W., Winkner U., Mewes H.W., Weill B. and Wiemann S.
EST (Ansoerge, W., Winkner, U., Mewes, H.W., Weill, B. and Wiemann, S.)
Unpublished (1999)
CONTACT: Ansoerge W
MIPS

Am Klopferpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.

This clone (DKEZP761O1814) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

FEATURES

source

1..669
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKEZP761O1814"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT 214 a 118 c 141 g 196 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.4e-23;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 tggaaagtgaacggatcgccacatttgaataaagaattgaagcctatataga 616

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OY      617  acctaaagaagaagaatctgttcccaagctataccaccaagtgctttagccctcaac 676
Db      61  ACCTTAAGAAGAAGAAATCTGTCTCCAGCTATACCAACCAAGTGTCTTTAGCCTTCAAC 120
OY      677  tttaga 681
Db      121  TTTGA 125
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